APPENDIX I

SHOWING MARKED-UP VERSION OF CLAIMS

21. A method of screening a patient perioperatively to determine a risk for complications during a surgical procedure associated with known genetic variations comprising:

a) obtaining a sample from a perioperative subject, said perioperative subject being a patient scheduled for a surgical procedure that has not yet completed said surgical procedure; and

b) subjecting said sample to an assay for detecting two or more nucleic acid genetic markers to generate a genomic profile for use in selecting a perioperative course of action, wherein said subjecting step occurs after said patient is scheduled for surgery but before completion of said surgical procedure, thereby determining a risk for complications during said surgical procedure.

30. The method of Claim 21, wherein said two or more nucleic acid genetic markers comprise mutations in two or more genes, said genes selected from the group consisting of BChE, CYP2D6, MTHFR, MS, CBS, F 5 Leiden, Prothrombin, RYR1, CACNA1S, and CPT2.

32. A method for selecting conditions for a surgical procedure by screening a patient perioperatively to determine a risk for complications during a surgical procedure associated with known genetic variations comprising:

a) providing a sample from a perioperative subject; and

b) subjecting said sample to an assay for detecting two or more nucleic acid genetic markers known to be associated with perioperative phenotypes to generate a genomic profile for use in selecting a surgical procedure treatment course of action; and

c) subjecting said subject to a surgical procedure, wherein conditions for said procedure are selected using said genomic profile.

36. The method of Claim 32, wherein said two or more nucleic acid genetic markers comprises a mutation in two or more genes, said genes selected from the group consisting of BChE, CYP2D6, MTHFR, MS, CBS, F 5 Leiden, Prothrombin, RYR1, CACNA1S, and CPT 2.

37. A method of screening a patient perioperatively to determine a risk for complications during a surgical procedure from known genetic variations comprising:

a) obtaining a sample from a perioperative subject; and

b) subjecting said sample to an assay for detecting two or more nucleic acid genetic markers clinically associated with two or more conditions selected from the group consisting of butyrylcholinesterase deficiency, poor debrisoquine metabolism, thrombus, and malignant hyperthermia to generate a genomic profile, wherein said genomic profile provides information for use by a physician in determining a risk for complications during a surgical procedure.